Lactose Transport System of *Streptococcus thermophilus*

THE ROLE OF HISTIDINE RESIDUES*

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The lactose transport protein (LacS) of *Streptococcus thermophilus* is a chimeric protein consisting of an amino-terminal carrier domain and a carboxyl-terminal phosphoenolpyruvate:sugar phosphotransferase system (PTS) IIA protein domain. The histidine residues of LacS were changed individually into glutamine or arginine residues. Of the 11 histidine residues present in LacS, only the His-376 substitution in the carrier domain significantly affected sugar transport. The region around His-376 was found to exhibit sequence similarity to the region around His-322 of the lactose transport protein (LacY) of *Escherichia coli*, which has been implicated in sugar binding and in coupling of sugar and H⁺ transport. The H376Q mutation resulted in a reduced rate of uptake and altered affinity for lactose (α-galactoside), melibiose (α-galactoside), and the lactose analog methyl-β-D-thiogalactopyranoside. Similarly, the extent of accumulation of the galactosides by cells expressing LacS(H376Q) was highly reduced in comparison to cells bearing the wild-type protein. Nonequilibrium exchange of lactose and protons and galactosides demonstrated using purified Enzyme I1 and I11 domains, respectively. The IIA protein domain of LacS contains 2 histidine residues (His-537 and His-552) that are conserved in the homologous PTSs and are phosphorylated by HPr(His-P) of various organisms. His-552 of LacS corresponds to His-91 of the IIA protein of *E. coli*, which has been shown to be phosphorylated by HPr(P) (Dorschug et al., 1984). The lactose transport protein (LacS) is a secondary active transport system that catalyzes the uptake of various α- and β-galactosides in symport with a proton as well as exchange of galactosides. The heterologous exchange of lactose for galactose most likely occurs during metabolism of lactose by *S. thermophilus* and *Lactobacillus bulgaricus* (Poolman, 1990).

Although the overall similarity between the carrier domain of LacS and the lactose carrier (LacY) of *E. coli* is not significant (Poolman et al., 1989), a region (H376/E379) in LacS can be identified that is similar to the H322/E325 region in LacY (Fig. 1). Evidence has been presented indicating that His-322, Glu-325 (putative helix X), and Arg-302 (putative helix IX) of LacY are in close contact with each other and that these residues could form a “charge relay” system that participates in the coupled transmembrane movement of protons and galactosides (Püttrner et al., 1986, 1988; Carrasco et al., 1986, 1989; Menick et al., 1987; Lee et al., 1988). Recently, the requirement of an ionizable histidine residue at position 322 in LacY for galactoside/proton symport has been questioned (King and Wilson, 1989a, 1989b, 1990; Franco and Brooker, 1991). It has been shown that some His-322 mutants of LacY, which do not build up a galactoside concentration gradient, catalyze galactoside-dependent proton transport (King and Wilson, 1989a, 1989b, 1990). Moreover, the H322N mutant of LacY still accumulates lactose against a concentration gradient, although the levels of accumulation are low compared to those of the wild-type strain (Franco and Brooker, 1991). In this study, we assess the role of the histidine residues in the carrier and IIA protein domains of the lactose transport protein of *S. thermophilus*. The results indicate that His-552 is phosphorylated by HPr(His─P) from *Bacillus subtulis*, but that the conserved histidine residues in the IIA protein domain of LacS are not essential for transport. His-376 in the carrier domain of LacS could serve a role similar to that of His-322 in LacY. The similarities and differences between the proposed active-site residues of LacS and LacY are discussed.

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† The abbreviations used are: PTS, phosphoenolpyruvate:sugar phosphotransferase system; TMG, methyl-β-D-thio-galactopyranoside.

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EXPERIMENTAL PROCEDURES

Bacterial Strains and Plasmids

Bacterial strains are described in Table I. The cells were grown aerobically in Luria broth at 37 °C (Sambrook et al., 1989) unless indicated otherwise. Plasmid pEKS8 containing a 4.1-kilobase EcoRI chromosomal DNA fragment of *S. thermophilus*, encoding the lactose transport protein (LacS), has been described (Poolman et al., 1989, 1990). For the construction of pSKE8, the 4.1-kilobase EcoRI fragment of pEKS8 was ligated in the EcoRI site of pBluescript IISK+ (Stratagene). Plasmid pAVL1 is pACYC177 that carries a 9.5-kilobase HindIII chromosomal fragment of *Klebsiella pneumoniae* KAY2026, carrying the nag operon, including nagE, which codes for IICBA-N-acetylglucosamine (Vogler et al., 1988).

Site-directed Mutagenesis

The mutagenic primers are listed in Table II. Site-directed mutagenesis was carried out by the method of Kunkel et al. (1987).

**Mutations in pSKE8**—Single-stranded uracil-containing DNA of pSKE8 was isolated from E. coli C1236 (dur-, ung+)/pSKE8 after infection with helper phage M13KQ7 (Sambrook et al., 1989). Closed-circular heteroduplex DNA with the desired mutations was synthesized *in vitro* as described (Kunkel et al., 1987) and transformed to *E. coli* JM101 (ung+). Plasmid DNA was isolated from a number of transformants, and plasmids bearing the desired mutation(s) were identified by digestion with restriction enzymes for which a site was lost or created by the mutagenesis (see Table II). Subsequently, mutations were verified by nucleotide sequencing of double-stranded DNA using the dideoxy chain termination method (Sanger et al., 1977) and a set of primers complementary to a region of lacS located 50-100 bases downstream or upstream of the mutation site. Each mutant was isolated independently at least twice.

Mutations in pEKS8—The 648-base pair KpnI-EcoRI fragment of pEKS8, comprising the carboxyl-terminal 323-base pair region of lacS, was ligated in the replicative form of M13mp18/M13mp19. Recombinant phage DNA was used to transfect E. coli C1236, and single-stranded uracil-containing M13mp18 or M13mp19 DNA, including the KpnI-EcoRI fragment, was synthesized. Synthesis of the complementary strand and screening of mutants were carried out as described above. The entire region of lacS was sequenced. Subsequently, the KpnI-EcoRI fragment of pEKS8 was exchanged for the corresponding fragment containing the desired mutation that was isolated from the replicative form of the M13 DNA.

Preparation of Cell Suspensions

Overnight cultures or exponentially grown cells (A600 = 0.4-0.8) were harvested by centrifugation, washed twice, and resuspended to a final protein concentration of 20-80 mg/ml in 50 mM potassium phosphate (pH 7.5), 5 mM magnesium sulfate (KPM buffer), and 0.5 mM NaEDTA, purified HPr (0.5 mg/ml) and Enzyme 1 (0.35 mg/ml), and [32P]P-enolpyruvate (Reizer et al., 1984). The phosphorylation reaction was carried out at 37 °C for 15 min in a total volume of 15 μl. The reaction was stopped by addition of an equal volume of Laemmli sample buffer (Laemmli, 1970), and proteins were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (12.5% acrylamide and 5% polyacrylamide gel electrophoresis (12.5% acrylamide and 5% polyacrylamide gel electrophoresis (12.5% acrylamide and 5% polyacrylamide gel electrophoresis). The phosphorylation reaction was stopped by rapid filtration as described above.

Transport Assays

Transport experiments were performed at 20, 30, or 37 °C as specified in the figure legends.

**Active Transport**—Cells were diluted to a final protein concentration of 0.6-1.2 mg/ml in KPM buffer containing 10 mM D-lithium lactate as the electron donor. After 2 min of pre-energization in the presence of oxygen, radiolabeled substrate was added; and at appropriate time intervals, the uptake reaction was stopped by addition of 2 ml of ice-cold 100 mM LiCl. Cells were collected by filtration on a 0.45-μm cellulose nitrate filter (Millipore Corp.) and washed with 2 ml of ice-cold LiCl.

**Efflux and Exchange**—Preloading of cells with sugars was achieved by incubation (overnight at 4 °C) of the concentrated washed cell suspensions with the appropriate concentration of radiolabeled galactoside in the presence of deoxyribonuclease I (20 μg/ml). The next day, potassium azide and carbonyl cyanide m-chlorophenylhydrazone were added to final concentrations of 30 mM and 50 μM, respectively; and the cells were incubated for another 2 h at room temperature essentially as described (King and Wilson, 1990). For efflux and exchange, 1-μl aliquots of concentrated cell suspension (50-80 mg/ml) were diluted into 500 μl of KPM buffer containing no substrates and unlabeled galactosides, respectively. The transport reaction was stopped by rapid filtration as described above.

Isolation of Membranes

For the isolation of inside-out membrane vesicles of *E. coli* T184, T184/pEKS8, T184/pEKS8(H552Q), T184/pEKS8(H537A), and T184/pEKS8(1548E/G556D), cells were lysed by a 2-fold passage through a French pressure cell (20,000 p.s.i.), and membranes were collected as described (Poolman et al., 1983). The membranes were washed and resuspended to 20-30 mg of protein/ml in 10 mM Tris-HCl (pH 7.5) containing 0.5 mM phenylmethylsulfonyl fluoride.

**Protein Purification**

Enzyme I and HPr of *B. subtilis* and *E. coli* were purified as described previously (Reizer et al., 1989, 1992).

Phosphorylation Assay

Inside-out membrane vesicles (5 mg/ml) were incubated in 50 mM Tris-HCl (pH 7.5) containing 5 mM MgCl2, 0.1 mM dithiothreitol, 0.5 mM NaEDTA, purified HPr (0.5 mg/ml) and Enzyme 1 (0.35 mg/ml), and [32P]P-enolpyruvate (Reizer et al., 1984). The phosphorylation reaction was carried out at 37 °C for 15 min in a total volume of 15 μl. The reaction was stopped by addition of an equal volume of Laemmli sample buffer (Laemmli, 1970), and proteins were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (12.5% acrylamide and 5% polyacrylamide gel electrophoresis). The phosphorylation reaction was stopped by rapid filtration as described above.

Table I

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DW1</td>
<td>lacI-, Δlac(ZY), Δmell(AB), strA</td>
<td>Wilson and Wilson (1987)</td>
</tr>
<tr>
<td>PPA209</td>
<td>Δmell(AB), strA</td>
<td>Postma (1987)</td>
</tr>
<tr>
<td>T184</td>
<td>lacI-Δlac(ZY), melA+, ΔmellB, strA</td>
<td>Teather et al. (1980)</td>
</tr>
<tr>
<td>LR2-162</td>
<td>Δlac(ZY), strA</td>
<td>Vogler et al. (1988)</td>
</tr>
<tr>
<td>LR2-167</td>
<td>ΔlacI, Δlac(ZY), melA+, ΔmellB, strA</td>
<td>Vogler et al. (1988)</td>
</tr>
<tr>
<td>JM101</td>
<td>lacI-Δlac(ZY), strA</td>
<td>Vogler et al. (1988)</td>
</tr>
<tr>
<td>CJ236</td>
<td>lacI+Δlac(ZY), strA</td>
<td>Yanisch-Perron et al. (1987)</td>
</tr>
<tr>
<td>HB101</td>
<td>lacI-Δlac(ZY), strA</td>
<td>Kunke et al. (1987)</td>
</tr>
<tr>
<td>a</td>
<td>lacI-, Δlac(ZY), Δmell(AB), strA</td>
<td>Boyer and Roulland-Dussoix (1969)</td>
</tr>
</tbody>
</table>

*P. W. Postma, unpublished data.*
Lactose Transport in S. thermophilus

Mutations in the lactose transport gene of S. thermophilus

The nucleotides changed by the site-directed mutagenesis are underlined. The nucleotide changes resulting in the desired amino acid substitution are indicated in boldface type. The last column indicates whether a new restriction was created or a restriction site was lost as a result of the mutagenic event(s).

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Sequence of mutagenic primer</th>
<th>Restriction analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td>H39Q</td>
<td>5'-TTTGTGACACTCAATTTGTTDAAACGGGGGATCCAAAG</td>
<td>New BamHI</td>
</tr>
<tr>
<td>H51Q</td>
<td>5'-GCAAATAGTCATCTGTCTATTAACT</td>
<td>Loss of SnaBI</td>
</tr>
<tr>
<td>H155Q</td>
<td>5'-CTCTGCTTCTCAGATCAGTCAAGAAGGGAAG</td>
<td>New XbaI</td>
</tr>
<tr>
<td>H375Q</td>
<td>5'-AACCGGGACAGCGGCTATCAGC</td>
<td>New FokI</td>
</tr>
<tr>
<td>H422Q</td>
<td>5'-AACACACACACACACCGTTTATACTTAACCTTGGA</td>
<td>Loss of HindIII</td>
</tr>
<tr>
<td>H457Q</td>
<td>5'-AGCAGGCTACGGCCAAGAATTGGAAGAATTGG</td>
<td>New BstXI</td>
</tr>
<tr>
<td>H466Q</td>
<td>5'-TGTGCAAAGGGCAGCAACCTGGTTAGCG</td>
<td>New Ssal</td>
</tr>
<tr>
<td>H502Q</td>
<td>5'-TCTCAAGTCTGGCAGTTTGCAATTGCTTA</td>
<td>New HinII</td>
</tr>
<tr>
<td>H537A</td>
<td>5'-TCCATCTGGCAGTTCAGTGTA</td>
<td>Loss of BstXI</td>
</tr>
<tr>
<td>H537R</td>
<td>5'-TCTACTCTGCCGTACCTTGGA</td>
<td>New KpnI</td>
</tr>
<tr>
<td>H552Q</td>
<td>5'-GCCTTATGCCAGTGTGCAATCGGTACCGTTAATCCTT</td>
<td>New AauI</td>
</tr>
<tr>
<td>H612Q</td>
<td>5'-GTGTCTCTTGCAATTTATACGCTGATTGAAGAATTGG</td>
<td>New ClaI</td>
</tr>
<tr>
<td>I548E/G556D</td>
<td>5'-AGATGGTTGTTGAAGTCTTTATCCAGCTGGCATCGATACATTACGTTAAC</td>
<td>New Sall</td>
</tr>
</tbody>
</table>

Polyacrylamide). The 32P-labeled proteins were identified by autoradiography.

Miscellaneous

[32P]-Enolpyruvate was prepared as described previously (Reizer et al., 1984). For the calculation of intracellular concentrations, a specific internal volume of 3 μl/mg of cell protein was used. Protein was measured by the method of Lowry et al. (1951) with bovine serum albumin as a standard. Plasmid DNA was isolated by the alkali lysis method (Birnboim and Doly, 1979). For sequencing of double-stranded DNA, plasmid DNA was further purified by one or two polyethylene glycol precipitation steps and additional phenol/chloroform extraction, followed by ethanol precipitation and desaturation by alkali treatment (Sambrook et al., 1989).

Materials

[carboxyl-14C]Benzoic acid (50 mCi/mmol), methyl-α-d-([U-14C]glucopyranoside (50 mCi/mmol), and α-glucose-1-[3H]lactose (57 mCi/mmol) was obtained from Du Pont-New England Nuclear. [3H]Methyl-β-d-thiogalactopyranoside (50 mCi/mmol) was obtained from Du Pont-New England Nuclear. [3H]Melibiose (3.2 Ci/mmol) was a generous gift of Dr. G. LeBlanc (Bassilana et al., 1987).

RESULTS

Histidine Mutagenesis—The lactose transport protein (LacS) of S. thermophilus contains 11 histidine residues (circled in Fig. 1A), of which 5 are present in the carrier domain and 6 in the IIA protein domain. Each of the histidine residues was replaced by site-directed mutagenesis with glutamine or arginine (Table II). Glutamine and arginine were chosen as replacements on the basis of amino acid similarity coefficients of the other mutants were not significantly affected.

Since LacS transports lactose as well as melibiose (α-galactoside), TMG, galactose, and other galactosides, the effects of the H376Q mutation on the uptake of these carbohydrates were compared (Fig. 3). To avoid metabolism of lactose and melibiose, transport studies were carried out with E. coli DW1 (ΔlacZY, ΔmelAB)/pSKE8(wild type) and DW1/pSKE8(H376Q). The kinetic parameters for lactose uptake by E. coli DW1 bearing the wild-type or H376Q mutant proteins were similar to those obtained with E. coli DW2 bearing the corresponding transport protein (Table II). The data presented in Fig. 3 show that uptake of melibiose and TMG was markedly more affected by the H376Q mutation than uptake of lactose. In fact, the uptake rates were too low to determine accurately the kinetic parameters of the H376Q mutant (Fig. 3, B and C, insets). The Kₗ values for uptake of lactose, melibiose, and TMG by LacS(wild type) were 0.7, 0.53, and 0.27 mM, respectively. The Vₘₐₓ values for uptake of lactose, melibiose, and TMG were 270, 140, and 60 nmol/min/mg of protein, respectively.

In contrast to transport of lactose (Fig. 3A), TMG was not accumulated against a concentration gradient by the H376Q mutant (Fig. 3C). To establish whether this difference indeed reflected differences in the ability to accumulate various sugars or whether the apparent failure to accumulate TMG was due to higher efflux by passive and/or facilitated diffusion, a number of experiments were carried out. First, efflux of TMG was analyzed by diluting [3H]TMG-loaded cells into buffer without TMG. No significant differences were observed between the wild-type and H376Q mutants (Fig. 4). Second, the level of accumulation of TMG by the wild-type and H376Q proteins was determined over a wide range of concentrations (5-165 μM) and at different pH values (5.5-8.0). If passive efflux of TMG, in combination with a reduced rate of uptake, affects the accumulation level, one might observe a significant

2 B. Poolman, unpublished data.
pneumoniae of lactose transport protein of S. thermophilus. The region corresponds to the loop and raffinose transport proteins of E. coli. The region corresponds to the loop that connects helices X and XI of LacS. Sources of sequences are as follows: E. coli (ec) RaIF, Aslanidis et al. (1989); K. pneumoniae (kp), LacY, Memmorrow et al. (1988); E. coli LacY, Büchel et al. (1988); S. thermophilus, (st) LacS, Poolman et al. (1989); L. bugaricus (lb) Lacs, Poolman et al. and E. coli MelB, Yazyu et al. (1984). C, Conserved residues in IIA protein domain of LacS. The region shown corresponds to the proposed phosphorylation site of LacS. Sources of sequences are as follows (see also B): Crr, Nelson et al. (1983); NagE, Rogers et al. (1988); HglS (also indicated as BglF), Schnetz et al. (1987); Streptococcus mutans (sm) SerA, Sato et al. (1989); and B. subtilis (bs) PtaG, Gonzé-Tréboul et al. (1989) and Sutrina et al. (1990). Residues corresponding to His-537 and His-552 in NagE, H554jli.569

Conserved residues in the IIA domain of LacS

Conserved residues in carrier domain of LacS

Conserved residues in carrier protein domain of LacS

Transport proteins, although raffinose (trisaccharide/galactoside) was a more effective inhibitor of LacS(H376Q) compared with LacS(wild type).

The data presented above describe the effect of H376Q substitution on uphill (Δp-driven) transport by the lactose carrier protein. Under these conditions, a complete translocation cycle includes binding and release of H+ and galactoside as well as reorientation of the loaded and unloaded binding sites. Since LacS also catalyzes an exchange reaction involving only binding and release of galactoside and reorientation of loaded binding sites, nonequilibrium exchange of TMG and lactose by the wild-type and H376Q transport proteins were compared (Figs. 4 and 5). For the exchange reaction, cells were preloaded with [14C]TMG or [14C]lactose and, following treatment with azide/carbonyl cyanide m-chlorophenylhydrazone (see “Experimental Procedures”), diluted 500-fold into buffers containing unlabeled TMG (or lactose) at concentrations ranging from 0 to 20 mM. Since the rate of net galactoside transport was negligible in these “energy-poisoned” cells (inferred from uptake by unloaded cells) (data not shown),
Lactose Transport in S. thermophilus

1. Lactose Transport in S. thermophilus

Fig. 2. Lactose uptake by E. coli DW2/pSKE8 wild-type and histidine LacS mutants. Cells were suspended in KPM buffer (pH 6.5) supplemented with 10 mM D-lithium lactate to a final protein concentration of 0.8 mg/ml. After 2 min of pre-energization, [14C]lactose was added to a final concentration of 10 μM, and uptake was assayed for different time intervals. Cells harvested in the stationary phase of growth were used; the assay temperature was 30 °C. HxQ, histidine mutants except H155Q and H376Q. ○, wild-type (WT) LacS; □, H155Q mutant; △, H376Q mutants. The shaded area denotes the results obtained with all other histidine mutants of LacS.

Table III

Kinetic parameters of lactose transport by wild-type and histidine LacS mutants

Experimental conditions were similar to those described in the legend to Fig. 3, except that lactose concentrations ranged from 10 μM to 1.6 mM.

<table>
<thead>
<tr>
<th>Mutation</th>
<th>K&lt;sub&gt;T&lt;/sub&gt; (mM)</th>
<th>V&lt;sub&gt;max&lt;/sub&gt; (nmol/min/mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>0.8</td>
<td>210</td>
</tr>
<tr>
<td>H39Q</td>
<td>1.0</td>
<td>163</td>
</tr>
<tr>
<td>H51Q</td>
<td>1.2</td>
<td>180</td>
</tr>
<tr>
<td>H155Q</td>
<td>1.1</td>
<td>215</td>
</tr>
<tr>
<td>H376Q</td>
<td>0.27</td>
<td>40</td>
</tr>
<tr>
<td>H429Q</td>
<td>1.1</td>
<td>214</td>
</tr>
<tr>
<td>H457Q</td>
<td>1.4</td>
<td>235</td>
</tr>
<tr>
<td>H466Q</td>
<td>0.6</td>
<td>150</td>
</tr>
<tr>
<td>H502Q</td>
<td>0.8</td>
<td>160</td>
</tr>
<tr>
<td>H537R</td>
<td>0.9</td>
<td>174</td>
</tr>
<tr>
<td>H552Q</td>
<td>1.0</td>
<td>180</td>
</tr>
</tbody>
</table>

The observed isotope exit reaction reflects the real exchange of galactoside. Fig. 4 shows that initially the release of [14C]TMG from the cell was monoexponential with a slope that depends upon the external TMG concentration. The exchange reaction catalyzed by the H376Q mutant was somewhat slower than that of the wild-type strain (the K<sub>T</sub> values for external TMG were very similar, i.e. between 0.6 and 1.0 mM). This can be seen more readily from the kinetic analysis of lactose<sub>i</sub>/lactose<sub>o</sub> exchange (Fig. 5). At an internal lactose concentration of 4.5 mM (see legend to Fig. 5), the exchange kinetics yielded K<sub>T</sub> values for external lactose of ~10 mM, which is about an order of magnitude higher than that of Δp-driven lactose uptake (Fig. 3 and Table III).

Role of IIA Protein Domain—The homology between the IIA protein domain of LacS and the IIA protein (domain) of the glucose, N-acetylglucosamine, β-glucoside, and sucrose PTSs (Fig. 1C) suggests that Enzyme I and HPr can catalyze P-enolpyruvate-dependent phosphorylation of His-552 of the lactose transport protein. The data presented in Fig. 2 and
varying from 10 pM to 1 mM. The assay temperature was 37 °C; the pEKS8 (ptsI-) were compared. The results obtained with the final protein concentrations were between wild type.

ary phase of growth were used. Initial rates of uptake were estimated uptake and exchange of lactose by DW2/pEKS8 and PPA209/[14C]TMG were added to final concentrations of 3 pM (multidrug efflux) or 0.1 (C), 0.4 (D), 2 (E), or (A) 10 mM TMG (nonequilibrium exchange). The assay temperature was 30 °C.

Table IV, on the other hand, indicate that the H552Q mutant were similar to those of the wild-type mutant (data not shown). Second, manipulation of the level of PTS phosphoprotein intermediates by addition of nonmetabolizable sugar analog methyl-α-D-glucopyranoside and 2-deoxy-D-glucose (Nelson et al., 1986) did not affect the lactose transport activities. Third, pEKS8 (lacs+) was unable to complement E. coli LM1 (crr-, nugE) with respect to transport of α-methyl-D-glucoside. In accordance with previous observations (Vogler et al., 1988), pAVL1 containing nugE was able to restore the uptake of α-methyl-D-glucoside in E. coli LM1 to ~20% of the wild-type activity (strain LR2-167). Fourth, by examining the sequences of the IIA protein(s) (domains) of the lactose transport proteins of S. thermophilus and L. bulgaricus and the PTS proteins indicated in Fig. 1C, two positions were identified at which the lactose transport proteins differed significantly from the PTS proteins, i.e. Ile-548 and Gly-556. These residues are close to proposed phosphorylation site residue (His-552); and the crystal structure of the IIA^{Glc} protein domain of the glucose PTS of B. subtilis indicates that the equivalent residues, i.e. Glu-79 and Asp-87, can assume a role in recognition of the interactive PTS proteins (the IIB protein domain or HPr) and facilitate the phosphoryl transfer reaction (Liau et al., 1991). The double mutant LacS(H548E/G556D) was constructed, but the I548E/G556D mutations did not affect lactose transport activity (data not shown).

Phosphorylation of Lactose Transport Protein—To establish whether LacS could be phosphorylated by HPr(His-P), inside-out membrane vesicles of E. coli T184/pKK223-3 (lacS-, vector control) and T184/pEKS8 (lacS+) and various mutants

<table>
<thead>
<tr>
<th>Sugar excess</th>
<th>LacS(wild type)</th>
<th>LacS(H376Q)</th>
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<tbody>
<tr>
<td></td>
<td>V_{lac}</td>
<td>V_{luc}</td>
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<tr>
<td>No additions</td>
<td>10.8 (100)</td>
<td>1.3 (100)</td>
</tr>
<tr>
<td>Lactose</td>
<td>0.7</td>
<td>&lt;0.1</td>
</tr>
<tr>
<td>Melibiose</td>
<td>0.7</td>
<td>&lt;0.1</td>
</tr>
<tr>
<td>TDG</td>
<td>0.4</td>
<td>&lt;0.1</td>
</tr>
<tr>
<td>Galactose</td>
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<td>&lt;0.1</td>
</tr>
<tr>
<td>Maltose</td>
<td>9.5</td>
<td>88</td>
</tr>
<tr>
<td>Sucrose</td>
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<td>IPTG</td>
<td>0.3</td>
<td>3</td>
</tr>
<tr>
<td>Raffinose</td>
<td>9.0</td>
<td>83</td>
</tr>
</tbody>
</table>

* TDG, β-D-galactopyranosyl-1-thio-β-D-galactopyranoside; IPTG, isopropyl-1-thio-β-D-galactopyranoside.
presented above, phosphorylation of LacS could not be de-
ected with Enzyme I and HPr isolated from E. coli, K. pneumoniae, S. thermophilus, and L. bulgaricus; the raffinose transport protein of E. coli; and the melibiose carrier of E. coli. Substitution of Glu-325 in LacY leads to a transport protein that does not catalyze lactose/H+ symport or lactose efflux, but catalyzes exchange and counterflow at normal rates (Carrasco et al., 1986). Similarly, substitution of the corresponding residue in MelB (Glu-361) for glycine, aspartate, or alanine affects sugar and cation translocation, but not recognition of the substrates (Pourcher et al., 1990b).

Mutations of the conserved lysine (Fig. 1B, arrow 2) have been isolated for LacY after selection for enhanced recognition of maltose (α-galactoside) and resistance for TDG (Collins et al., 1989). The LacY(K319N) mutant protein exhibits diminished recognition of β-galactosides and β-glucosides. The conserved acidic residue corresponding to arrow 1 (Fig. 1B) has not been investigated in any of the transport proteins. Overall, comparison of the sequences presented in Fig. 1B and the data obtained from mutagenesis experiments suggests that the region connecting helixes X and XI of LacS is important for substrate recognition.

A difference worth noting between the LacS and LacY regions is the higher polarity of the residues around His-376 (LacS) in comparison to the region around His-322 (LacY). As a consequence, hydrophathy analysis predicts the His-322 region of LacY to be in the membrane, whereas the His-376 region of LacS is predicted to be in a cytoplasmic loop. Nevertheless, the local environment of the important residues in both protein segments might be similar if the regions are located near the head groups of the lipid bilayer.

The effect of the H376Q substitution on galactoside transport by LacS has been analyzed by measuring Δp-driven uptake and exchange under nonequilibrium conditions. Assuming that the Vmax of the exchange reaction reflects the level of expression of the lactose transport protein, the effect of the H376Q mutation on the kcat of Δp-driven uptake is ~2-fold smaller than indicated by the Vmax values for uptake of lactose, melibiose, and TMG (Fig. 3). The observation that Δp-driven transport of galactosides is more severely affected by the His-376 mutation than the exchange reaction suggests that the histidine at position 376 is important for energy transduction, i.e. coupled movement of galactosides and protons. The results also indicate that His-376 is not obligatorily

\(^5\) V. Swarte and B. Poolman, unpublished data.
required for the active accumulation of galactosides.

The in vitro phosphorylation assays indicated that LacS can be phosphorylated by HPr(His-P) of  B. subtilis and that His-552 in the IIA protein domain is most likely the phosphorylation site. Nevertheless, the in vivo transport experiments that were performed in  E. coli bearing LacS did not provide an indication regarding the functional and/or regulatory role(s) of the phosphorylation reaction. Although  B. subtilis IIA GIC can readily replace  E. coli IIA GIC with respect to sugar transport and regulation (Reizer et al., 1992), it is possible that the IIA protein domain of LacS is a poor phosphoryl acceptor and/or phosphoryl donor of the  E. coli HPr(His-P) and/or the IIB GLC domain, respectively. Consequently, discerning the role of LacS phosphorylation may require the use of PTS systems derived from homologous systems (or other Gram-positive bacteria) rather than the heterologous system used in the in vivo studies described here. In addition, we cannot exclude the possibility that phosphorylation of the IIA protein domain of LacS does not play a direct role in the translocation of lactose across the membrane, but rather functions in the intracellullarily formed glucose following hydrolysis of the incoming lactose. Guided by these suppositions, a study is now underway to examine the role of LacS phosphorylation in  S. thermophilus.

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REFERENCES


Lactose Transport in  S. thermophilus